





PubMed	Nucleotide	Protein	Genome	Structure	Popset
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☐ 1: Gl = "7484807" [GenPept]

AMP deaminase homolog F16M1...

BLink, Related Sequences, Taxonomy

LOCUS T01259 600 aa PLN 14-MAY-1999

DEFINITION AMP deaminase homolog F16M14.21 - Arabidopsis thaliana.

ACCESSION T01259 PID q7484807

VERSION T01259 GI:7484807 DBSOURCE pir: locus T01259;

summary: #length 600 #molecular-weight 69656 #checksum 4877;

genetic: #map_position 2 #introns 64/3; 82/1; 124/3; 184/3; 207/2; 255/1; 275/3; 313/3; 360/3; 411/3; 429/3; 466/3; 524/3; 551/3 #note

F16M14.21;

PIR dates: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change

14-May-1999.

KEYWORDS

SOURCE thale cress.

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core

eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;

Arabidopsis.

REFERENCE 1 (residues 1 to 600)

AUTHORS Rounsley, S.D., Kaul, S., Lin, X., Ketchum, K.A., Crosby, M.L.,

Brandon, R.C., Sykes, S.M., Mason, T.M., Kerlavage, A.R., Adams, M.D.,

Somerville, C.R. and Venter, J.C.

TITLE Direct Submission

JOURNAL Submitted (??-JUL-1998) to the EMBL Data Library

FEATURES Location/Qualifiers

source 1..600

/organism="Arabidopsis thaliana"

/db xref="taxon:3702"

Protein 1..600

/product="AMP deaminase homolog F16M14.21"

ORIGIN

1 miclevptsd eveaykclqe clelrkryvf qetvapweke visdpstpkp ntepfahypq 61 gksdhcfemq dgvvhvfank dakedlfpva datafftdlh hvlkviaagn irtlchrrlv 121 lleqkfnlhl mlnadkefla qksaphrdfy nvrkvdthvh hsacmnqkhl lrfiksklrk 181 epdevvifrd gtyltlrevf esldltgydl nvdlldvhad kstfhrfdkf nlkynpcgqs 241 rlreiflkqd nliqgrflge itkqvfsdle askyqmaeyr isiygrkmse wdqlaswivn 301 ndlysenvvw liqlprlyni ykdmgivtsf qnildnifip lfeatvdpds hpqlhvflkq 361 vvgfdlvdde skperrptkh mptpaqwtna fnpafsyyvy ycyanlyvln klreskgmtt 421 itlrphsgea gdidhlaatf ltchsiahgi nlrkspvlqy lyylaqigla msplsnnslf 481 ldyhrnpfpv fflrglnvsl stddplqihl tkeplveeys iaasvwklsa cdlceiarns 541 vyqsgfshal kshwigkdyy krgpdgndih ktnvphirve frdtvwneiy lfftqvnfsl

601

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